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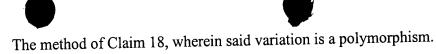


- 1. A composition comprising an isolated nucleic acid, wherein said nucleic acid comprises a sequence that shares at least 96% identity with SEQ ID NO:1 or the complement of SEQ ID NO:1.
 - 2. The composition of Claim 1, wherein said sequence shares at least 97% identity with SEQ ID NO:1 or the complement of SEQ ID NO:1.
- 10 3. The composition of Claim 1, wherein said sequence shares at least 98% identity with SEQ ID NO:1 or the complement of SEQ ID NO:1.
 - 4. The composition of Claim 1, wherein said sequence is operably linked to a heterologous promoter.
 - 5. The composition of Claim 1, wherein said sequence is contained within a vector.

6. A composition comprising an isolated peptide encoded by the sequence of Claim 1.

- 7. A composition comprising an isolated nucleic acid, wherein said nucleic acid comprises a sequence encoding a peptide that shares at least 96% identity with SEQ ID NO:3.
- 8. The composition of Claim 7, wherein said peptide shares at least 97% identity with SEQ ID NO:3.
- 9. The composition of Claim 7, wherein said peptide shares at least 98% identity with SEQ ID NO:3.
 - 10. The composition of Claim 7, wherein said sequence is operably linked to a heterologous promoter.

The composition of Claim 7, wherein said sequence is contained within a 11. vector. A composition comprising an isolated peptide encoded by the sequence of 5 Claim 7. A composition comprising an isolated peptide, wherein said peptide comprises 13. an amino acid sequence that shares at least 96% identity with SEQ ID NO:3. 10 The composition of Claim 13, wherein said amino acid sequence shares at 14. least 97% identity with SEQ ID NO:3. The composition of Claim 13, wherein said amino acid sequence shares at 15. least 98% identity with SEQ ID NO3. 15 A composition comprising an isolated nucleic acid, wherein said nucleic acid 16. comprises SEQ ID NO:1 or the complement of SEQ ID NO:1. composition comprising an isolated peptide, wherein said peptide comprises 20 SEQ ID N A method for determining the risk of eye disease comprising: 18. providing nucleic acid from a subject, wherein said nucleic acid LPH gene; and comprises an 25 detecting the presence or absence of at least one variation in said LPH b) gene. The method of Claim 18, further comprising step c) providing a diagnosis to 19. said subject based on the presence or absence of said variation. 30 The method of Claim 18, wherein said variation is a mutation. 20.



22. The method of Claim 18, wherein said LPH gene is selected from human LPH1, human LPH2, and human LPH3.

The method of Claim 18, wherein said LPH gene is a human LPH3 sequence, and said variation prevents the peptide encoded by said human LPH3 sequence from binding the human TIGR peptide.

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